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RAW SEQUENCE LISTING

DATE: 10/29/2001

PATENT APPLICATION: US/09/787,126

TIME: 15:35:51

Input Set : A:\2001-10-09 3631-0108P.txt
Output Set: N:\CRF3\10292001\I787126.raw

4 <110> APPLICANT: M&E Biotech A/S
5 HALKIER, Torben
6 HAANING, Jesper
8 <120> TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand
9 Activity
11 <130> FILE REFERENCE: 3631-0108P
13 <140> CURRENT APPLICATION NUMBER: US 09/787,126
C--> 14 <141> CURRENT FILING DATE: 2001-10-09 *of*
16 <160> NUMBER OF SEQ ID NOS: 36
18 <170> SOFTWARE: PatentIn Ver. 2.1
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 2271
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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32 cgcacacaag aaggggaggg agcgggagag ggaggagagc tccgaagcga gaggggccgag 180
33 cgcc atg cgc cgc gcc agc aga gac tac acc aag tac ctg cgt ggc tcg 229
34 Met Arg Arg Ala Ser Arg Asp Tyr Thr Lys Tyr Leu Arg Gly Ser
35 1 5 10 15
36 gag gag atg ggc ggc ccc gga gcc ccg cac gag ggc ccc ctg cac 277
37 Glu Glu Met Gly Gly Pro Gly Ala Pro His Glu Gly Pro Leu His
38 20 25 30
39 gcc ccg ccg cct gcg ccg cac cag ccc ccc gcc tcc cgc tcc 325
40 Ala Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser
41 35 40 45
42 atg ttc gtg gcc ctc ctg ggg ctg ggg ctg ggc cag gtt gtc tgc agc 373
43 Met Phe Val Ala Leu Leu Gly Leu Gly Gln Val Val Cys Ser
44 50 55 60
45 gtc gcc ctg ttc tat ttc aga gcg cag atg gat cct aat aga ata 421
46 Val Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
47 65 70 75
48 tca gaa gat ggc act cac tgc att tat aga att ttg aga ctc cat gaa 469
49 Ser Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu
50 80 85 90 95
51 aat gca gat ttt caa gac aca act ctg gag agt caa gat aca aaa tta 517
52 Asn Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu
53 100 105 110
54 ata cct gat tca tgt agg aga att aaa cag gcc ttt caa gga gct gtg 565
55 Ile Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val
56 115 120 125
57 caa aag gaa tta caa cat atc gtt gga tca cag cac atc aga gca gag 613
58 Gln Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu

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61	Lys Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys			
62	145	150	155	
63	ctt gaa gct cag cct ttt gct cat ctc act att aat gcc acc gac atc			709
64	Leu Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile			
65	160	165	170	175
66	cca tct ggt tcc cat aaa gtg agt ctg tcc tct tgg tac cat gat cgg			757
67	Pro Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg			
68	180	185	190	
69	ggt tgg gcc aag atc tcc aac atg act ttt agc aat gga aaa cta ata			805
70	Gly Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile			
71	195	200	205	
72	gtt aat cag gat ggc ttt tat tac ctg tat gcc aac att tgc ttt cga			853
73	Val Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg			
74	210	215	220	
75	cat cat gaa act tca gga gac cta gct aca gag tat ctt caa cta atg			901
76	His His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met			
77	225	230	235	
78	gtg tac gtc act aaa acc agc atc aaa atc cca agt tct cat acc ctg			949
79	Val Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu			
80	240	245	250	255
81	atg aaa gga gga agc acc aag tat tgg tca ggg aat tct gaa ttc cat			997
82	Met Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His			
83	260	265	270	
84	ttt tat tcc ata aac gtt ggt gga ttt ttt aag tta cgg tct gga gag			1045
85	Phe Tyr Ser Ile Asn Val Gly Phe Phe Lys Leu Arg Ser Gly Glu			
86	275	280	285	
87	gaa atc agc atc gag gtc tcc aac ccc tcc tta ctg gat ccg gat cag			1093
88	Glu Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln			
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90	gat gca aca tac ttt ggg gct ttt aaa gtt cga gat ata gat tga			1138
91	Asp Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp			
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93	cccccagttt ttggagtgtt atgtatttcc tggatgtttt gaaacatttt taaaaacaag			1198
94	ccaaagaaga tgtatataagg tggatgtttt gaaacatttt taaaaacaag 1198			1258
95	actcagtatc catgctttt accttggata gaacacgcgt attacagcc agtgggagat			1318
96	gttagactca tggatgtttt cacaatggtt tttttttt gtaatgaatt cctagaattt			1378
97	aaccatggatc gagcaattac gggttgcac tatgagaaac tgcatgtggg ctatgggagg			1438
98	gttgttccc tggatgtttt ccccttcgcac gctgaagtgg agagggtgtc atctagcgca			1498
99	atggatcatcttgcac ttgttgcac ccctggggaa aacttgcac taaggagggg			1558
100	aaaaaaatcttctaatg aggagagaaa atatatgtat ttttatataa tatctaaagt			1618
101	tatatttcag atgtatgtt ttctttgcac agtattgtaa attatattt tgctatagta			1678
102	tttgattcaa aatatttataa aatgttgc tggatgtttt ttaatgttt taaatgtaca			1738
103	gacatattta actgggtgcac ttgttgcac ccctggggaa aacttgcac taaggagggg			1798
104	aaaaaaatgt tggatgttttccatcataatgc agtattttt ttcgttcttt ttaatgttt			1858
105	agattttttc agacttgcac agcctgtgc aaaaaattaa aatggatgcc ttgaataataa			1918
106	agcaggatgt tggccaccag gtgccttc aattttagaaa ctaatttgact tttagaaagct			1978
107	gacattgcca aaaaggatac ataatgggcc actgaaatct gtcaagagta gttatataat			2038

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108 tggtaaacag gtgttttcc acaagtgcgg caaattgtac ctttttttt ttttcaaaaat 2098
 109 agaaaaggta tttagtggttt atcagaaaaa aagtccaaatt ttaattttagt aaatgttatac 2158
 110 ttatactgtt caataaaaaac attgcctttg aatgttaatt ttttggtaaca aaaataaaatt 2218
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 115 <211> LENGTH: 317
 116 <212> TYPE: PRT
 117 <213> ORGANISM: Homo sapiens
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 123 20 25 30
 124 Pro Pro Pro Ala Pro His Gln Pro Pro Ala Ala Ser Arg Ser Met
 125 35 40 45
 126 Phe Val Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser Val
 127 50 55 60
 128 Ala Leu Phe Phe Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile Ser
 129 65 70 75 80
 130 Glu Asp Gly Thr His Cys Ile Tyr Arg Ile Leu Arg Leu His Glu Asn
 131 85 90 95
 132 Ala Asp Phe Gln Asp Thr Thr Leu Glu Ser Gln Asp Thr Lys Leu Ile
 133 100 105 110
 134 Pro Asp Ser Cys Arg Arg Ile Lys Gln Ala Phe Gln Gly Ala Val Gln
 135 115 120 125
 136 Lys Glu Leu Gln His Ile Val Gly Ser Gln His Ile Arg Ala Glu Lys
 137 130 135 140
 138 Ala Met Val Asp Gly Ser Trp Leu Asp Leu Ala Lys Arg Ser Lys Leu
 139 145 150 155 160
 140 Glu Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Thr Asp Ile Pro
 141 165 170 175
 142 Ser Gly Ser His Lys Val Ser Leu Ser Ser Trp Tyr His Asp Arg Gly
 143 180 185 190
 144 Trp Ala Lys Ile Ser Asn Met Thr Phe Ser Asn Gly Lys Leu Ile Val
 145 195 200 205
 146 Asn Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His
 147 210 215 220
 148 His Glu Thr Ser Gly Asp Leu Ala Thr Glu Tyr Leu Gln Leu Met Val
 149 225 230 235 240
 150 Tyr Val Thr Lys Thr Ser Ile Lys Ile Pro Ser Ser His Thr Leu Met
 151 245 250 255
 152 Lys Gly Gly Ser Thr Lys Tyr Trp Ser Gly Asn Ser Glu Phe His Phe
 153 260 265 270
 154 Tyr Ser Ile Asn Val Gly Gly Phe Phe Lys Leu Arg Ser Gly Glu Glu
 155 275 280 285
 156 Ile Ser Ile Glu Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp
 157 290 295 300
 158 Ala Thr Tyr Phe Gly Ala Phe Lys Val Arg Asp Ile Asp
 159 305 310 315

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178 <222> LOCATION: (454)..(948)
179 <223> OTHER INFORMATION: Tumour Necrosis Factor(TNF)-like domain
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185 gag atg ggc agc ggc ccc ggc gtc cca cac gag ggt ccg ctg cac ccc 96
186 Glu Met Gly Ser Gly Pro Gly Val Pro His Glu Gly Pro Leu His Pro
187 20 25 30
188 gcg cct tct gca ccg gct ccg gcg cca ccc gcc gcc tcc cgc tcc 144
189 Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser
190 35 40 45
191 atg ttc ctg gcc ctc ctg ggg ctg gga ctg ggc cag gtg gtc tgc agc 192
192 Met Phe Leu Ala Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser
193 50 55 60
194 atc gct ctg ttc ctg tac ttt cga gcg cag atg gat cct aac aga ata 240
195 Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile
196 65 70 75 80
197 tca gaa gac agc act cac tgc ttt tat aga atc ctg aga ctc cat gaa 288
198 Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu
199 85 90 95
200 aac gca ggt ttg cag gac act ctg gag agt gaa gac aca cta cct 336
201 Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro
202 100 105 110
203 gac tcc tgc agg agg atg aaa caa gcc ttt cag ggg gcc gtg cag aag 384
204 Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys
205 115 120 125
206 gaa ctg caa cac att gtg ggg cca cag cgc ttc tca gga gct cca gct 432
207 Glu Leu Gln His Ile Val Gly Pro Gln Arg Phe Ser Gly Ala Pro Ala
208 130 135 140
209 atg atg gaa ggc tca tgg ttg gat gtg gcc cag cga ggc aag cct gag 480
210 Met Met Glu Gly Ser Trp Leu Asp Val Ala Gln Arg Gly Lys Pro Glu
211 145 150 155 160
212 gcc cag cca ttt gca cac ctc acc atc aat gct gcc agc atc cca tcg 528
213 Ala Gln Pro Phe Ala His Leu Thr Ile Asn Ala Ala Ser Ile Pro Ser
214 165 170 175

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Input Set : A:\2001-10-09 3631-0108P.txt
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218	gcc aag atc tct aac atg acg tta agc aac gga aaa cta agg gtt aac	624
219	Ala Lys Ile Ser Asn Met Thr Leu Ser Asn Gly Lys Leu Arg Val Asn	
220	195 200 205	
221	caa gat ggc ttc tat tac ctg tac gcc aac att tgc ttt cggtt cat cat	672
222	Gln Asp Gly Phe Tyr Tyr Leu Tyr Ala Asn Ile Cys Phe Arg His His	
223	210 215 220	
224	gaa aca tcg gga agc gta cct aca gac tat ctt cag ctg atg gtg tat	720
225	Glu Thr Ser Gly Ser Val Pro Thr Asp Tyr Leu Gln Leu Met Val Tyr	
226	225 230 235 240	
227	gtc gtt aaa acc agc atc aaa atc cca agt tct cat aac ctg atg aaa	768
228	Val Val Lys Thr Ser Ile Lys Ile Pro Ser Ser His Asn Leu Met Lys	
229	245 250 255	
230	gga ggg agc acg aaa aac tgg tcg ggc aat tct gaa ttc cac ttt tat	816
231	Gly Gly Ser Thr Lys Asn Trp Ser Gly Asn Ser Glu Phe His Phe Tyr	
232	260 265 270	
233	tcc ata aat gtt ggg gga ttt ttc aag ctc cga gct ggt gaa gaa att	864
234	Ser Ile Asn Val Gly Phe Phe Lys Leu Arg Ala Gly Glu Glu Ile	
235	275 280 285	
236	agc att cag gtg tcc aac cct tcc ctg ctg gat ccg gat caa gat gcg	912
237	Ser Ile Gln Val Ser Asn Pro Ser Leu Leu Asp Pro Asp Gln Asp Ala	
238	290 295 300	
239	acg tac ttt ggg gct ttc aaa gtt cag gac ata gac tga	951
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254	Ala Pro Ser Ala Pro Ala Pro Pro Pro Ala Ala Ser Arg Ser	
255	35 40 45	
256	Met Phe Leu Ala Leu Leu Gly Leu Gly Leu Gly Gln Val Val Cys Ser	
257	50 55 60	
258	Ile Ala Leu Phe Leu Tyr Phe Arg Ala Gln Met Asp Pro Asn Arg Ile	
259	65 70 75 80	
260	Ser Glu Asp Ser Thr His Cys Phe Tyr Arg Ile Leu Arg Leu His Glu	
261	85 90 95	
262	Asn Ala Gly Leu Gln Asp Ser Thr Leu Glu Ser Glu Asp Thr Leu Pro	
263	100 105 110	
264	Asp Ser Cys Arg Arg Met Lys Gln Ala Phe Gln Gly Ala Val Gln Lys	
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VERIFICATION SUMMARY

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date